

SUPPLEMENTARY DATA

TABLE S1. Primers used for amplifying and sequencing

Primer name	Direction	PCR, sequencing	Primer sequence 5'-3'	Source
<u>rpoC1</u>				
rpoC1-1f	Forward	PCR,Seq	GTGGATACACTTCTTGATAATGG	http://www.kew.org/barcoding/protocols.html
rpoC1-3r	Reverse	PCR,Seq	TGAGAAAACATAAGTAAACGGGC	http://www.kew.org/barcoding/protocols.html
<u>rpoB</u>				
rpoB-1f	Forward	PCR,Seq	AAGTGCATTGTTGGAAC TGG	http://www.kew.org/barcoding/protocols.html
rpoB-4r	Reverse	PCR,Seq	GATCCCAGCATCACAATTC	http://www.kew.org/barcoding/protocols.html
<u>matK</u>				
matK-Xf	Forward	PCR,Seq	TAATTTACGATCAATTCATTC	http://www.kew.org/barcoding/update.html
matK-3.2r	Reverse	PCR,Seq	CTTCCTCTGTAAAGAATTC	http://www.kew.org/barcoding/protocols.html
matK-S571f	Forward	Seq	CATATAAACCAATTATCAAAC	This study (internal primer)
matK-S571r	Reverse	Seq	AGTTTGATAATTGGTTTATATG	This study (internal primer)
<u>trnH-psbA</u>				
psbA	Forward	PCR,Seq	GTTATGCATGAACGTAATGCTC	(Shaw et al. 2005)
trnH ^{GUG}	Reverse	PCR,Seq	CGCGCATGGTGGATTCACAATCC	(Shaw et al. 2005)
<u>trnQ-rps16</u>				
trnQ-S1f	Forward	PCR,Seq	GCGTGGCCAAGTGTAAGGC	modified from trnQ ^(UUG) (Shaw et al. 2007)
rps16-S1r	Reverse	PCR,Seq	GTTGCTTTCTACCACATCGTTT	modified from rps16x1 (Shaw et al. 2007)
trnQ-S801f	Forward	Seq	AACTCTTGATACTCGAGAAGAAGTG	this study (internal primer for Sisyrinchium)
trnQ-S493r	Reverse	Seq	TACGCCCCGTTATTTGGACTTTC	this study (internal primer for Sisyrinchium)
trnQ-OS896f	Forward	Seq	TTTCGGTTAAGTCAAAGGAGG	this study (internal primer for outgroups)
trnQ-O343r	Reverse	Seq	GTACAAGCATGCCCTGAATG	this study (internal primer for Olsynium)
trnQ-So874r	Reverse	Seq	CCCTTTGAGTTAACCGAAAGGCATTG	this study (internal primer for Solenomelus)
<u>nad1-2/3</u>				
nad1E2-1f	Forward	PCR,Seq	ACAGAGGATGTGCTCGTACGG	this study
nad1I2-465r	Reverse	Seq	TCGTCCATTCGTTGGGTGATC	this study (internal primer)
nad1I2-871r	Reverse	Seq	GCCCTAAGAAGCAGAACGCAC	this study (internal primer)
nad1I2-801f	Forward	Seq	CGTTTTTCATTTCTGGAAGTCC	this study (internal primer)
nad1E3-1r	Reverse	PCR,Seq	GCGCCATGACAATCTCACTCG	this study
<u>nad4-1/2</u>				
nad4E1-1f	Forward	PCR,Seq	GAAAGCGTGCCAATCCCTATG	this study
nad4I1-400r	Reverse	Seq	CCTGGTCGGGTACAGTTTCC	this study (internal primer)
nad4I1-936r	Reverse	Seq	CGGCCTGTAGACACATGTAAG	this study (internal primer)
nad4I1-824f	Forward	Seq	GGCGACCATAACATAAGGCAATG	this study (internal primer)
nad1I1-1283f	Forward	Seq	CCTGAGAAGGGAGTGGCTACC	this study (internal primer)
nad4E2-1r	Reverse	PCR,Seq	GCCAAGATGACGGATCCTGC	this study
<u>ITS</u>				
ITS5b	Forward	PCR,Seq	GGAAGTAAAAGTCGTAACAAG	modified from ITS5 (White et al., 1990)
ITS-38f	Forward	PCR,Seq	CTGCGGAAGGATCATTGTC	this study
ITS4	Reverse	PCR,Seq	TCCTCCGCTTATTGATATGC	(White et al., 1990)

Seq = sequencing

TABLE S2. PCR profiles for DNA amplification

Locus	PCR profiles
rpoC	Initial denaturation at 94°C for 1 mn followed by 40 cycles of 94°C denaturation for 30 s, 53°C annealing for 40 s and
rpoB	72°C elongation for 40 s, followed by a final elongation step of 5 mn at 72°C. (http://www.kew.org/barcoding/protocols.html).
matK	
psbA-trnH	
trnQ-rps16	Initial denaturation at 94°C for 5 mn followed by 40 cycles of 94°C denaturation for 30 s, 62°C annealing for 40 s and 72°C elongation for 1 mn 30 s, followed by a final elongation step of 5 mn at 72°C. (http://www.kew.org/barcoding/protocols.html).
nad1-2/3	Initial denaturation at 94°C for 5 mn followed by 40 cycles of 94°C denaturation for 1 mn, 65°C annealing for 40 s and 72°C elongation for 2 mn, followed by a final elongation step of 5 mn at 72°C.
nad4-1/2	Initial denaturation at 94°C for 5 mn followed by 40 cycles of 94°C denaturation for 1 mn, 64°C annealing for 40 s and 72°C elongation for 2 mn, followed by a final elongation step of 5 mn at 72°C.
ITS	Initial denaturation at 94°C for 5 mn followed by 40 cycles of 94°C denaturation for 1 mn, 58°C annealing for 1 mn and 72°C elongation for 1 mn, followed by a final elongation step of 5 mn at 72°C.

TABLE S3. Data and models used in analysis

Data partition	No. of positions without primers	Partition by codon position*	Model	
			ML	BI
rpoC1	508	X	GTR+I	GTR+I
rpoB	472	X	GTR	GTR
matK	1024	X	GTR+G	GTR+G
<u>trnH-psbA</u>	667		HKY+I+G	
psbA	53	X		K80
psbA-rps19 spacer	160			GTR+G
rps19 (negative strand)	279	X		HKY+I
rps19-trnH spacer	175			F81+I
trnQ-rps16	1929		GTR+G	GTR+G
cpDNA combined matrix			GTR+I+G	
nad1-2/3	1657		GTR+I	
5'-nad1-exon2	59			F81
nad1-exon2	82	X		HKY
nad1-intron2	1516			GTR+I
nad4-1/2	1683		GTR+I+G	
nad4-intron1	1406			GTR+I+G
nad4-exon2	277	X		HKY+I
mtDNA combined matrix			GTR+I+G	
<u>ITS</u>	665		GTR+I+G	
ITS1	225			GTR+G
5.8S	165			K80
ITS2	234			GTR+G
28S	41			K80+I
Global combined matrix			GTR+I+G	

* Partitioned by codon position = partition treated as a coding partition in bayesian analysis.